

## SEQUENCE LISTING

<110> Micromet AG  
 <120> Compositions comprising polypeptides  
 <130> MIC-017 PCT  
 <150> EP 03 027 511.9  
 <151> 2003-11-28  
 <160> 6  
 <170> PatentIn version 3.1  
 <210> 1  
 <211> 504  
 <212> PRT  
 <213> artificial sequence  
 <220>  
 <223> Construct 1: VL(CD19)-VH(CD19)-VH(CD3)-VL(CD3)  
 <400> 1  
 Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly  
 1 5 10 15  
 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp  
 20 25 30  
 Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro  
 35 40 45  
 Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro  
 50 55 60  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His  
 65 70 75 80  
 Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr  
 85 90 95  
 Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly  
 100 105 110  
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val  
 115 120 125  
 Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val  
 130 135 140  
 Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met  
 145 150 155 160  
 Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln  
 165 170 175  
 Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly  
 180 185 190  
 Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln  
 195 200 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg  
 210 215 220  
 Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp  
 225 230 235 240  
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp  
 245 250 255  
 Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser  
 260 265 270  
 Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr  
 275 280 285  
 Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly  
 290 295 300  
 Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys  
 305 310 315 320  
 Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met  
 325 330 335  
 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala  
 340 345 350  
 Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr  
 355 360 365  
 Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly  
 370 375 380  
 Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro  
 385 390 395 400  
 Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg  
 405 410 415  
 Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly  
 420 425 430  
 Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly  
 435 440 445  
 Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu  
 450 455 460  
 Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln  
 465 470 475 480  
 Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu  
 485 490 495  
 Leu Lys His His His His His  
 500

<210> 2  
 <211> 505  
 <212> PRT  
 <213> artificial sequence

&lt;220&gt;

&lt;223&gt; Construct 2: VH(CD19) -VL(CD19) -VH(CD3) -VL(CD3)

&lt;400&gt; 2

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr  
 20 25 30  
 Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe  
 50 55 60  
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr  
 65 70 75 80  
 Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp  
 100 105 110  
 Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly  
 115 120 125  
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr  
 130 135 140  
 Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile  
 145 150 155 160  
 Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu  
 165 170 175  
 Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr  
 180 185 190  
 Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser  
 195 200 205  
 Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val  
 210 215 220  
 Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr  
 225 230 235 240  
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Gly Gly Gly Gly Ser  
 245 250 255  
 Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala  
 260 265 270  
 Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr  
 275 280 285  
 Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
 290 295 300  
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe

305					310					315					320
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
				325					330					335	
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
			340					345					350		
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly
		355					360					365			
Thr	Thr	Leu	Thr	Val	Ser	Ser	Val	Glu	Gly	Gly	Ser	Gly	Gly	Ser	Gly
	370					375					380				
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser
385					390					395					400
Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys
				405					410					415	
Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser
			420					425					430		
Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser
		435					440					445			
Gly	Val	Pro	Tyr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser
	450					455					460				
Leu	Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys
465					470					475					480
Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu
				485					490					495	
Glu	Leu	Lys	His	His	His	His	His	His							
			500					505							

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<210> 3
<211> 504
<212> PRT
<213> artificial sequence
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<220>
<223> Construct 6: VH(CD3) -VL(CD3) -VH(CD19) -VL(CD19)
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<400> 3

Asp 1	Ile	Lys	Leu 5	Gln	Gln	Ser	Gly	Ala 10	Glu	Leu	Ala	Arg	Pro	Gly 15	Ala
Ser	Val	Lys	Met 20	Ser	Cys	Lys	Thr	Ser 25	Gly	Tyr	Thr	Phe	Thr 30	Arg	Tyr
Thr	Met	His 35	Trp	Val	Lys	Gln	Arg 40	Pro	Gly	Gln	Gly	Leu 45	Glu	Trp	Ile
Gly	Tyr	Ile	Asn 50	Pro	Ser	Arg 55	Gly	Tyr	Thr	Asn	Tyr 60	Asn	Gln	Lys	Phe
Lys 65	Asp	Lys	Ala	Thr 70	Leu	Thr	Thr	Asp	Lys	Ser 75	Ser	Ser	Thr	Ala	Tyr 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 115 120 125  
 Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile  
 130 135 140  
 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 145 150 155 160  
 Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser  
 165 170 175  
 Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro  
 180 185 190  
 Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 195 200 205  
 Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 210 215 220  
 Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 225 230 235 240  
 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu  
 245 250 255  
 Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly  
 260 265 270  
 Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly  
 275 280 285  
 Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr  
 290 295 300  
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu  
 305 310 315 320  
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp  
 325 330 335  
 Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg  
 340 345 350  
 Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val  
 355 360 365  
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 370 375 380  
 Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu  
 385 390 395 400  
 Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr  
 405 410 415  
 Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro

420                      425                      430  
 Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro  
           435                      440                      445  
 Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile  
           450                      455                      460  
 His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser  
           465                      470                      475                      480  
 Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
                           485                      490                      495  
 Ser Gly His His His His His His  
                           500

<210> 4  
 <211> 503  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> Construct 8: VH(CD3)-VL(CD3)-VL(CD19)-VH(CD19)

<400> 4

Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala  
 1                      5                      10                      15  
 Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr  
           20                      25                      30  
 Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
           35                      40                      45  
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe  
           50                      55                      60  
 Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr  
           65                      70                      75                      80  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
           85                      90                      95  
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly  
           100                      105                      110  
 Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
           115                      120                      125  
 Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile  
           130                      135                      140  
 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
           145                      150                      155                      160  
 Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser  
           165                      170                      175  
 Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro  
           180                      185                      190

Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 195 200 205  
 Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 210 215 220  
 Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 225 230 235 240  
 Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser  
 245 250 255  
 Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser  
 260 265 270  
 Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln  
 275 280 285  
 Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu  
 290 295 300  
 Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 305 310 315 320  
 Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr  
 325 330 335  
 His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr  
 340 345 350  
 Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
 355 360 365  
 Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val  
 370 375 380  
 Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala  
 385 390 395 400  
 Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly  
 405 410 415  
 Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr  
 420 425 430  
 Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser  
 435 440 445  
 Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala  
 450 455 460  
 Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr  
 465 470 475 480  
 Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 485 490 495  
 Gly His His His His His His  
 500

<210> 5  
 <211> 504  
 <212> PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; Construct 5: VL(CD3)-VH(CD3)-VH(CD19)-VL(CD19)

&lt;400&gt; 5

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1           5           10           15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
          20           25           30

Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
          35           40           45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser
          50           55           60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65           70           75           80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
          85           90           95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly
          100          105          110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser
          115          120          125

Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys
          130          135          140

Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln
145          150          155          160

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg
          165          170          175

Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr
          180          185          190

Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr
          195          200          205

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His
          210          215          220

Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
225          230          235          240

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu
          245          250          255

Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
          260          265          270

Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
          275          280          285

Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
          290          295          300

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Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu  
 305 310 315 320  
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp  
 325 330 335  
 Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg  
 340 345 350  
 Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val  
 355 360 365  
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 370 375 380  
 Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu  
 385 390 395 400  
 Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr  
 405 410 415  
 Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro  
 420 425 430  
 Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro  
 435 440 445  
 Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile  
 450 455 460  
 His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser  
 465 470 475 480  
 Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 485 490 495  
 Ser Gly His His His His His  
 500

&lt;210&gt; 6

&lt;211&gt; 503

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; Construct 7: VL(CD3)-VH(CD3)-VL(CD19)-VH(CD19)

&lt;400&gt; 6

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly  
 1 5 10 15  
 Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met  
 20 25 30  
 Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr  
 35 40 45  
 Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser  
 50 55 60  
 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu  
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr  
 85 90 95  
 Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly  
 100 105 110  
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser  
 115 120 125  
 Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys  
 130 135 140  
 Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln  
 145 150 155 160  
 Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg  
 165 170 175  
 Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr  
 180 185 190  
 Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr  
 195 200 205  
 Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His  
 210 215 220  
 Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser  
 225 230 235 240  
 Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser  
 245 250 255  
 Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser  
 260 265 270  
 Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln  
 275 280 285  
 Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu  
 290 295 300  
 Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 305 310 315 320  
 Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr  
 325 330 335  
 His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr  
 340 345 350  
 Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
 355 360 365  
 Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val  
 370 375 380  
 Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala  
 385 390 395 400  
 Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly  
 405 410 415

Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr  
420 425 430

Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser  
435 440 445

Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala  
450 455 460

Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr  
465 470 475 480

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
485 490 495

Gly His His His His His His  
500